

FIG. 1A

5' GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT

 ATA GAA TTA **ATG** GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA

 M E S R K D I T N Q E E L W K

 ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA

 M K P R R N L E E D D Y L H K D T G

 GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT

 E T S M L K R P V L L H L H Q T A H

 GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA

 A D E F D C P S E L Q H T Q E L F P

 CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT

Q W H L P I K I A A I I A S L T F L

 TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT

Y T L L R E V I H P L A T S H Q Q Y

 TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC

 F Y K I P I L V I N K V L P M V S I

 ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT

T L L A L V Y L P G V I A A I V Q L

 CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA

 H N G T K Y K K F P H W L D K W M L

 ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT

 T R K Q F G L L S F F F A V L H A I

 TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG

Y S L S Y P M R R S Y R Y K L L N W

GCA	TAT	659	CAA	CAG	GTC	668	CAA	CAA	AAT	677	AAA	GAA	GAT	686	GCC	TGG	ATT	695	GAG	CAT	GAT	704	GTT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A	Y	Q	Q	V	Q	Q	N	K	E	D	A	W	I	E	H	D	V						
TGG	AGA	713	ATG	GAG	ATT	722	TAT	GTG	TCT	731	CTG	GGA	ATT	740	GTG	GGA	TTG	749	GCA	ATA	CTG	758	GCT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
W	R	M	E	I	<u>Y</u>	<u>V</u>	<u>S</u>	<u>L</u>	<u>G</u>	<u>I</u>	<u>V</u>	<u>G</u>	<u>L</u>	<u>A</u>	<u>I</u>	<u>L</u>	<u>A</u>						
CTG	TTG	767	GCT	GTG	ACA	776	TCT	ATT	CCA	785	TCT	GTG	AGT	794	GAC	TCT	TTG	803	ACA	TGG	AGA	812	GAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
<u>L</u>	<u>L</u>	<u>A</u>	<u>V</u>	<u>T</u>	<u>S</u>	<u>I</u>	<u>P</u>	<u>S</u>	<u>V</u>	S	D	S	L	T	W	R	E						
TTT	CAC	821	TAT	ATT	CAG	830	AGC	AAG	CTA	839	GGA	ATT	GTT	848	TCC	CTT	CTA	857	CTG	GGC	ACA	866	ATA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
F	H	Y	I	<u>Q</u>	<u>S</u>	<u>K</u>	<u>L</u>	<u>G</u>	<u>I</u>	<u>V</u>	<u>S</u>	<u>L</u>	<u>L</u>	<u>L</u>	<u>G</u>	<u>T</u>	<u>I</u>						
CAC	GCA	875	TTG	ATT	TTT	884	GCC	TGG	AAT	893	AAG	TGG	ATA	902	GAT	ATA	AAA	911	CAA	TTT	GTA	920	TGG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
<u>H</u>	<u>A</u>	<u>L</u>	<u>I</u>	<u>F</u>	<u>A</u>	<u>W</u>	<u>N</u>	<u>K</u>	W	I	D	I	K	Q	F	V	W						
TAT	ACA	929	CCT	CCA	ACT	938	TTT	ATG	ATA	947	GCT	GTT	TTC	956	CTT	CCA	ATT	965	GTT	GTC	CTG	974	ATA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y	T	P	P	T	F	<u>M</u>	<u>I</u>	<u>A</u>	<u>V</u>	<u>F</u>	<u>L</u>	<u>P</u>	<u>I</u>	<u>V</u>	<u>V</u>	<u>L</u>	<u>I</u>						
TTT	AAA	983	AGC	ATA	CTA	992	TTC	CTG	CCA	1001	TGC	TTG	AGG	1010	AAG	AAG	ATA	1019	CTG	AAG	ATT	1028	AGA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
<u>F</u>	<u>K</u>	<u>S</u>	<u>I</u>	<u>L</u>	<u>F</u>	<u>L</u>	<u>P</u>	<u>C</u>	<u>L</u>	R	K	K	I	L	K	I	R						
CAT	GGT	1037	TGG	GAA	GAC	1046	GTC	ACC	AAA	1055	ATT	AAC	AAA	1064	ACT	GAG	ATA	1073	TGT	TCC	CAG	1082	TTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
H	G	W	E	D	V	T	K	I	N	K	T	E	I	C	S	Q	L						
TAG	AAT	1091	TAC	TGT	TTA	1100	CAC	ACA	TTT	1109	TTG	TTC	AAT	1118	ATT	GAT	ATA	1127	TTT	TAT	CAC	1136	CAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
*	N	Y	C	L	H	T	F	L	F	N	I	D	I	F	Y	H	Q						
CAT	TTC	1145	AAG	TTT	GTA	1154	TTT	GTT	AAT	1163	AAA	ATG	ATT	1172	ATT	CAA	GGA	1181	AAA	AAA	AAA	1190	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
H	F	K	F	V	F	V	N	K	M	I	I	Q	G	K	K	K	K						

AAA AA 3'

K

FIG. 1B

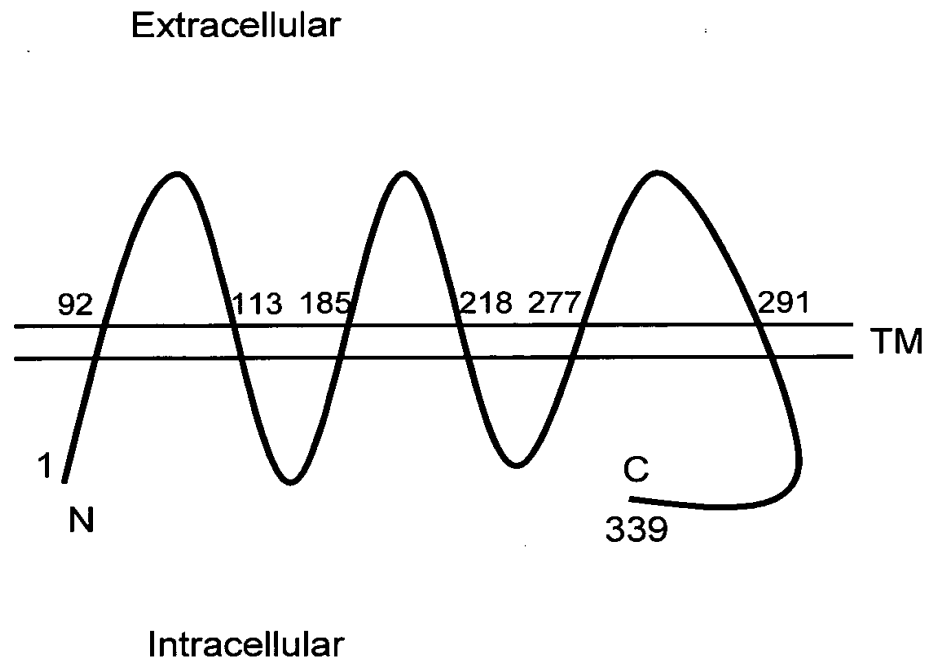
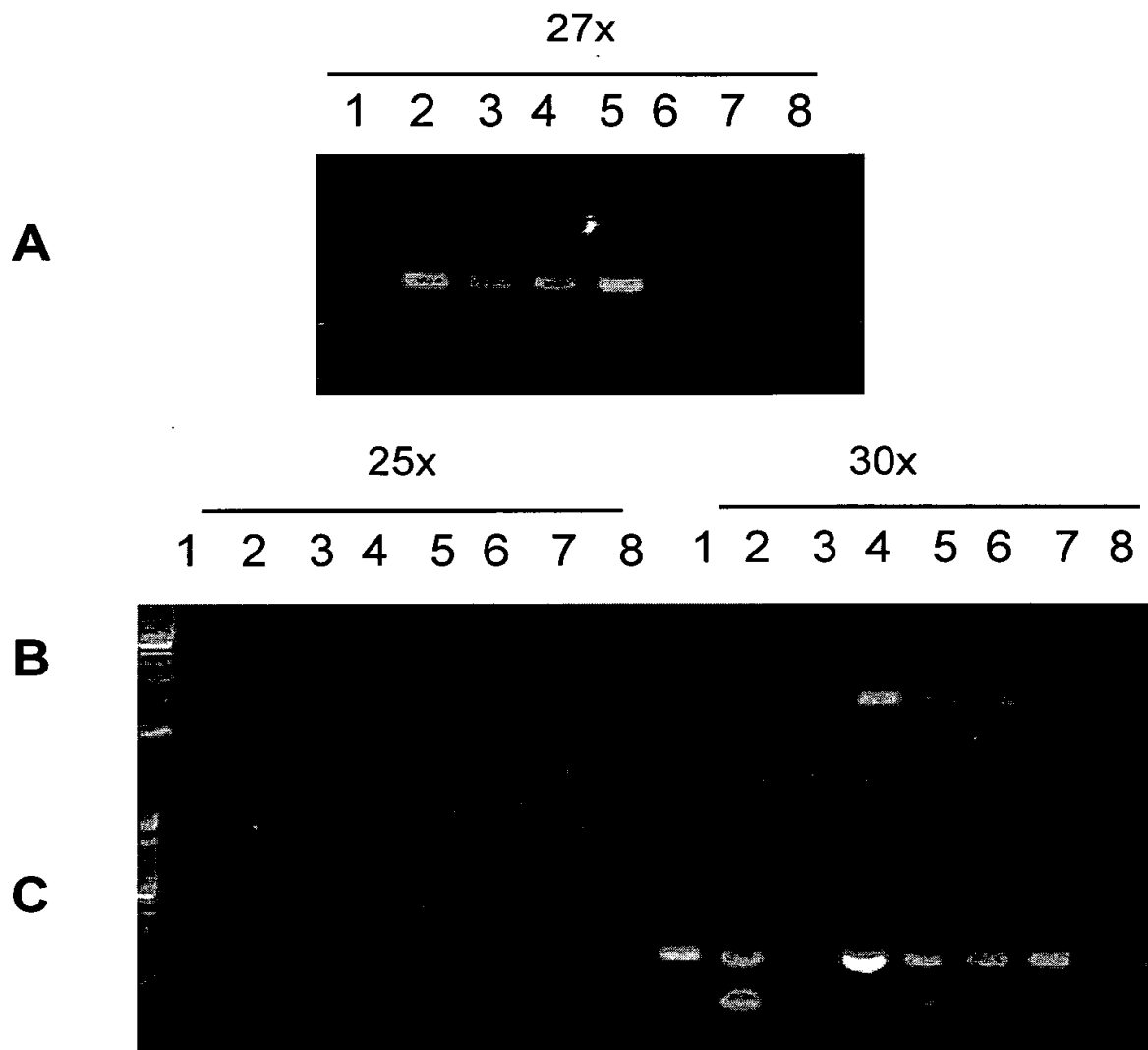


FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3'

FIG. 2



Panels:

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A

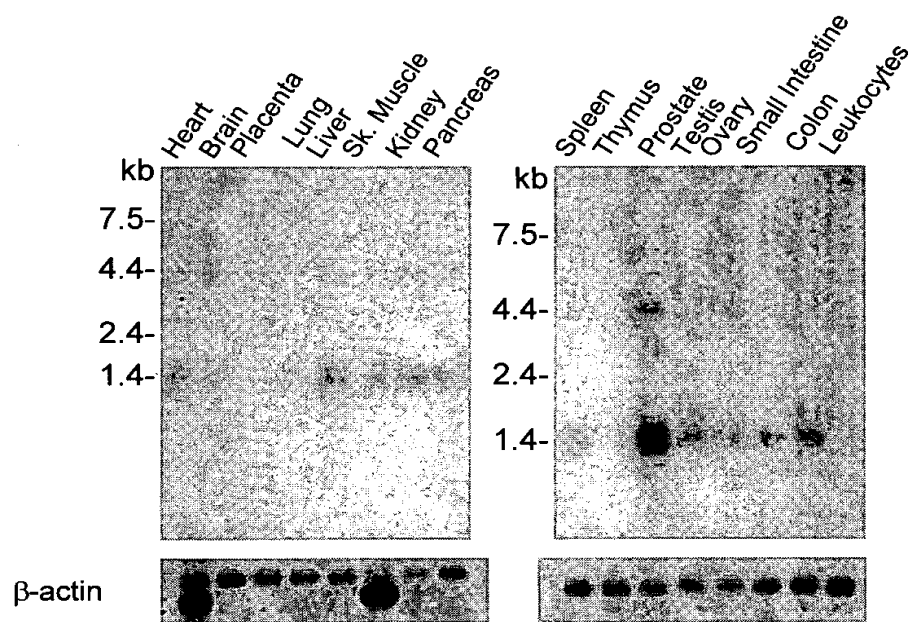


FIG. 3B

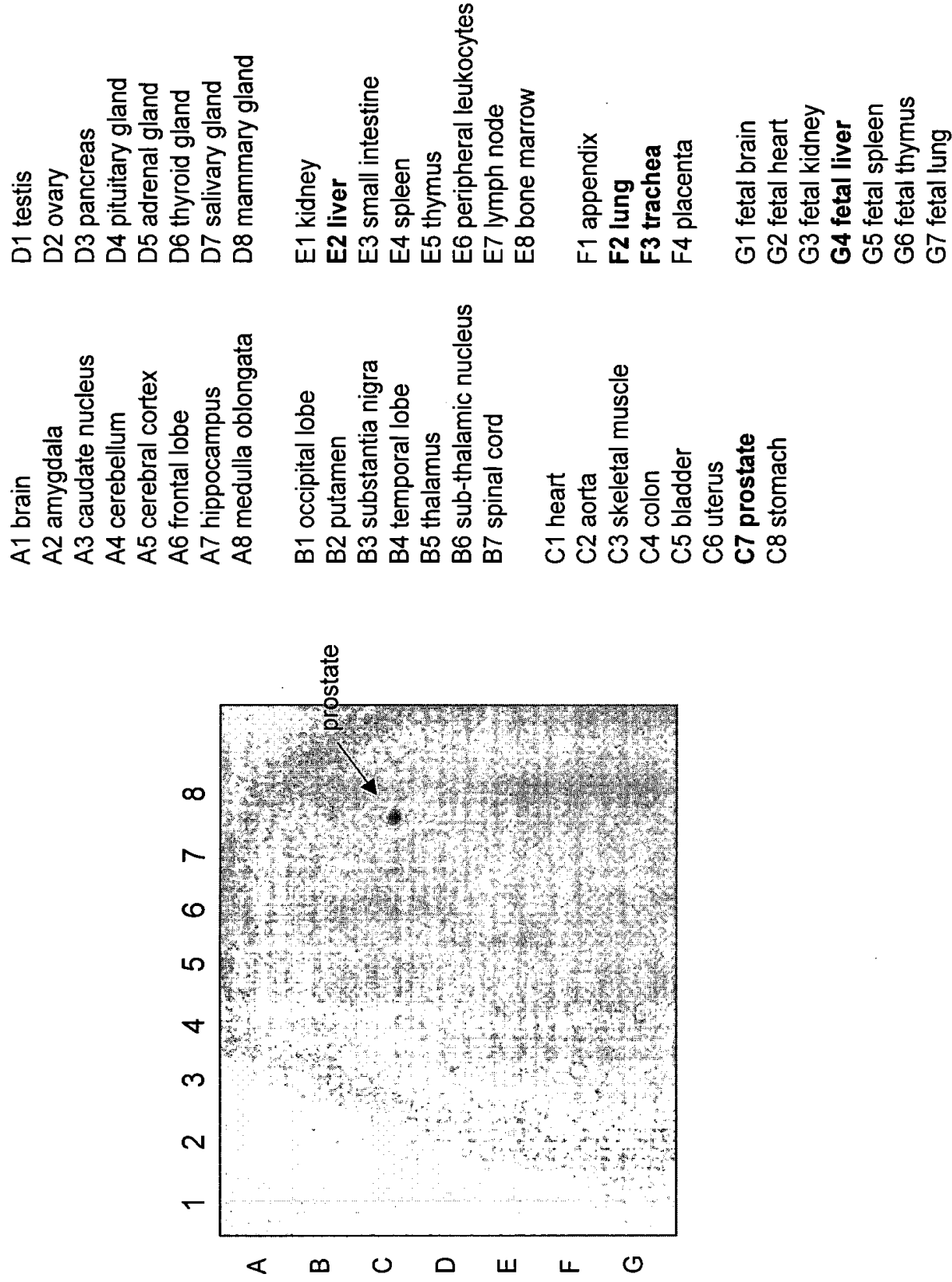


FIG. 4

GGGGCCCCGACCTCTGGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA
GTGGCACTTGCCAATTAATAAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAA
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATAACAAGTTGCTAAACTGGGCAT
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG
AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT
ATAGAATATGTTGACTTTACCCCATAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCTAGACATAAATAAAGGCAT
TAAATATTCTTTGTTTTTTTTTTTTTTGTTTGTTGTTTTTTGTTTGTTGTTGTTTTTTGAGATGAAGTCTCG
CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATT
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTA
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCACCTCGGCCTCCC
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT
GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACC
TGTACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTTAGCACTTTCAGAAACAAAACTCTCTCCTTGAAA
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGCTGTGACAAGATTCAAAGGACTAAA
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTGGAATTTCCACAAGGTCAGACATT
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAGTATGC
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTAATTTTGTAGGTTT
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA
TGAACACTGCTTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACCTGAGCCTATTCTACTATATGTACA

ATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTCAACT
AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAAGTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA
ACGCAAACCTAGCTATTTGATTGTATTCAGTGGGACTTAAAGATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGTTCAGAAGTCGTATAAAAGAGGTGTTGTGAGAACACCGT
TGAGATTACATAGGTGAACAACATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT
TTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAAGCACAAAAAATAAATATCATAAG
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG
TTCAGTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAGAGCAGAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTCTTTTGCAGAGCAAGCTAGGA
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG
TATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATT
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAATTAACAAAACCTGAG
ATATGTTCCAGTTGTAGAAATTACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCAACATTTCA
AGTTTGTATTTGTTAATAAAATGATTATCAAGGAAAAAAAAAAAAAAAAAAAAA

FIG. 5

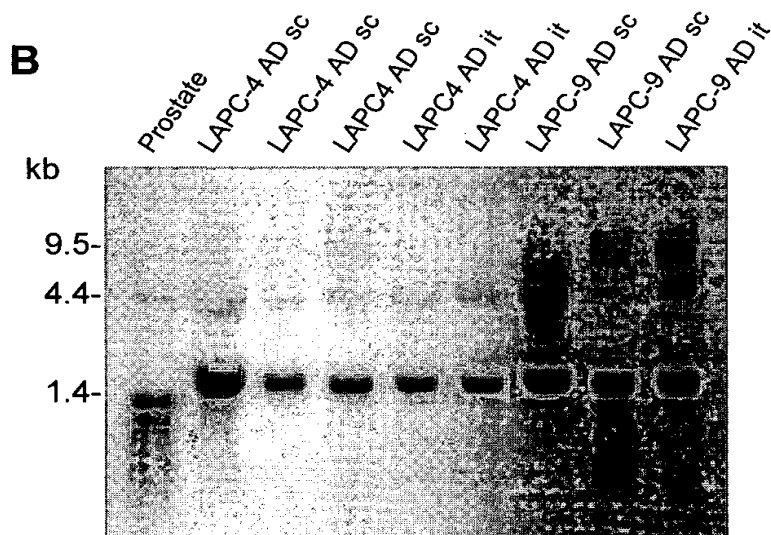
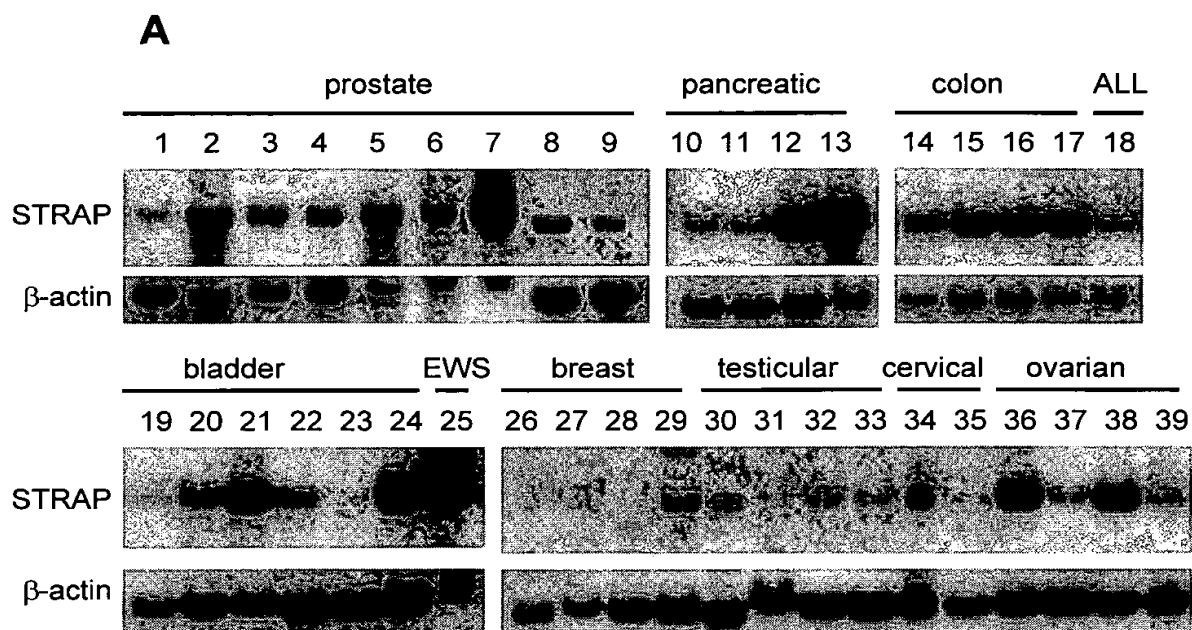


FIG. 6

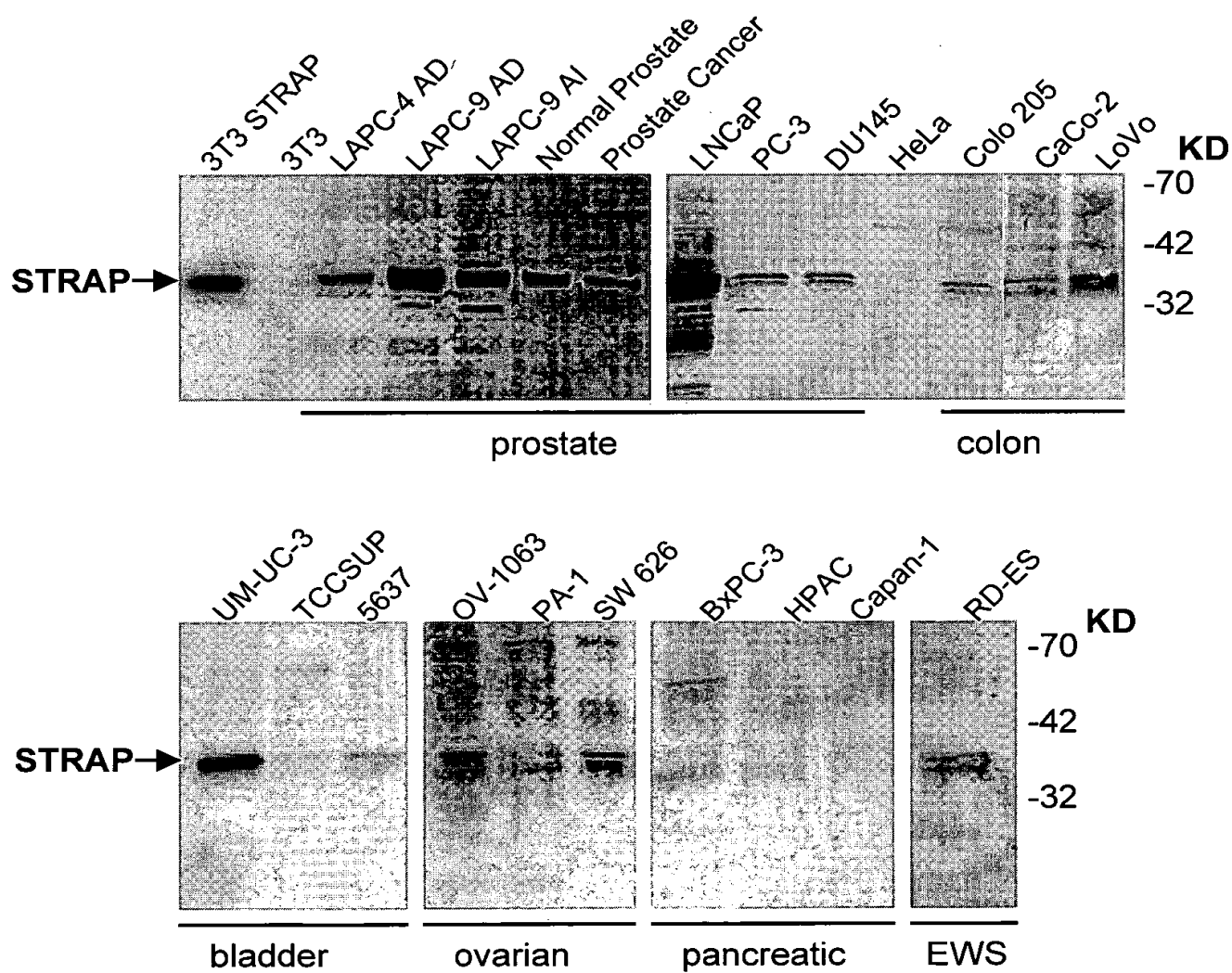
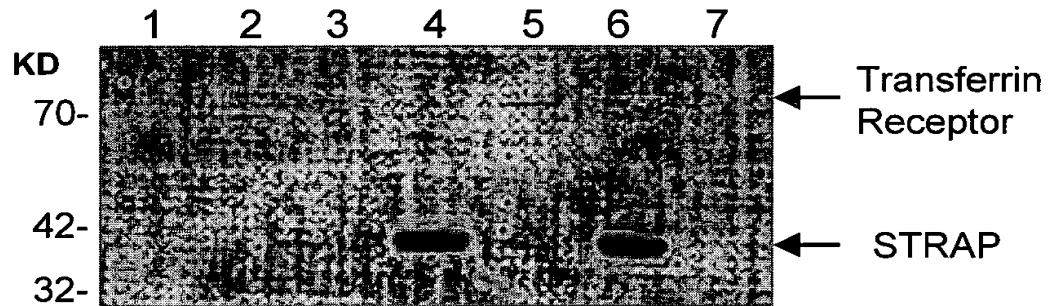


FIG. 7

A



B

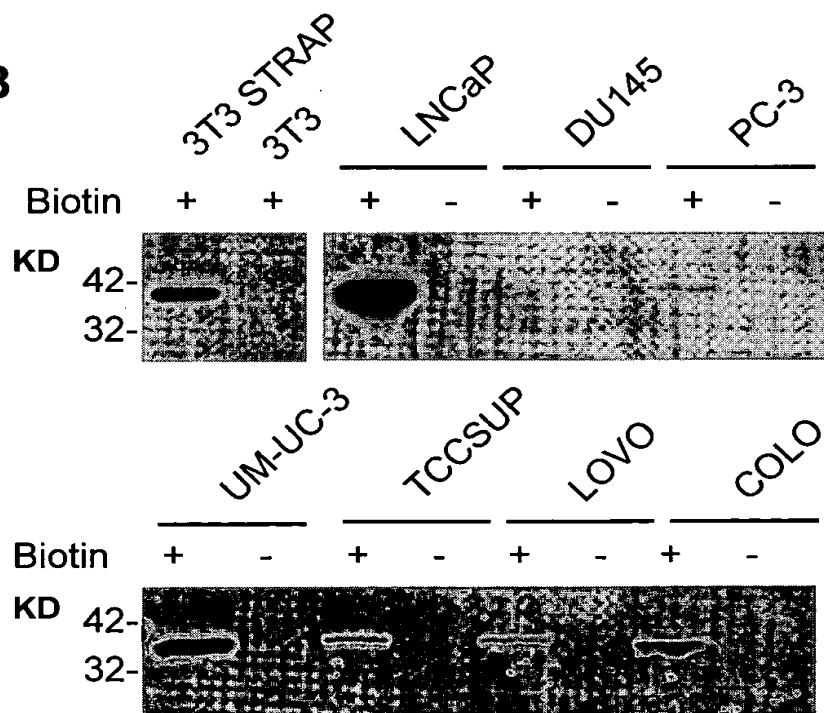


FIG. 8

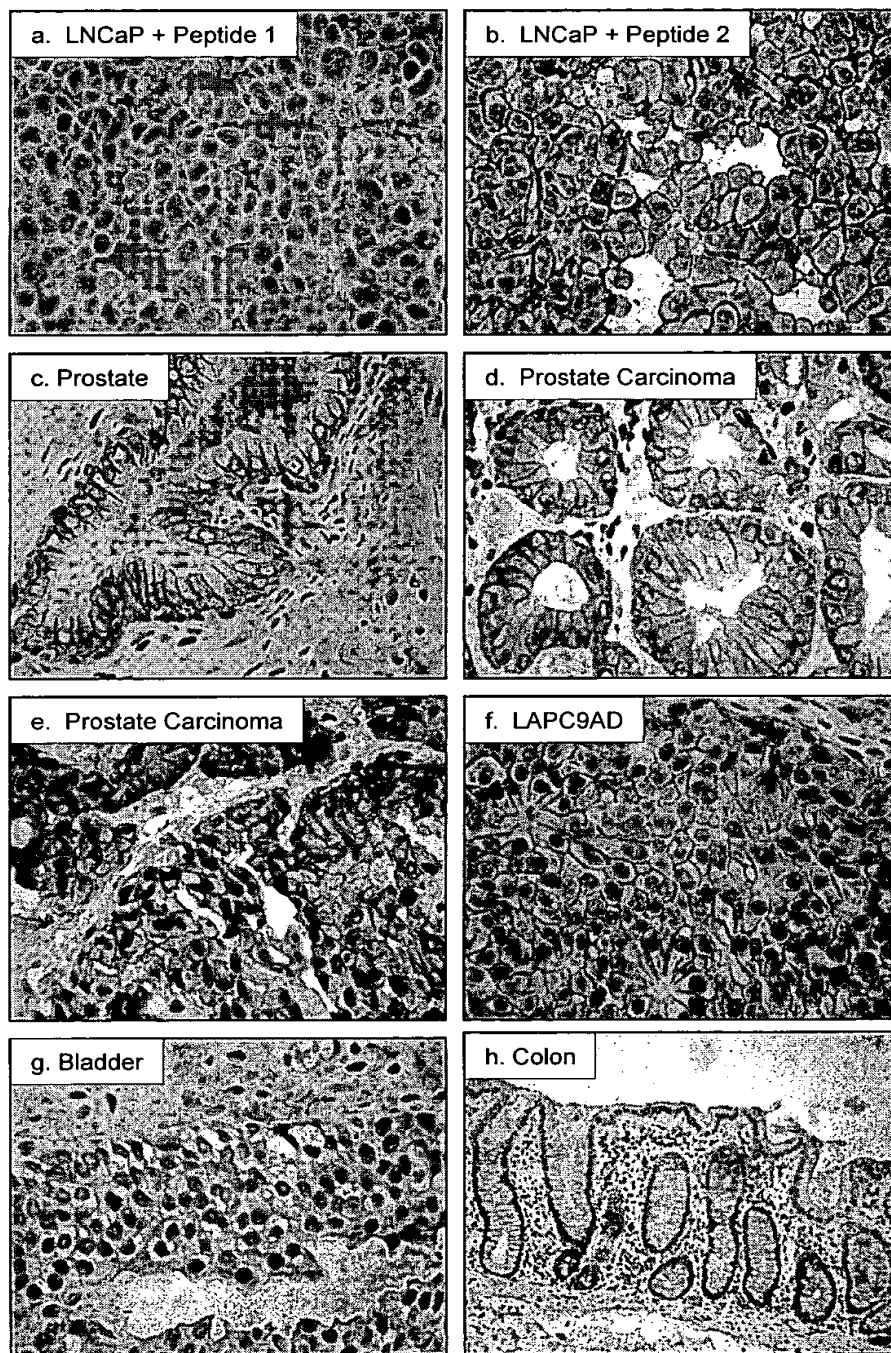


FIG. 9

5'	10			19			28			37			46			55		
	GGA	CGC	GTG	GGC	GGA	CGC	GTG	GGT	TCC	TCG	GGC	CCT	CGG	CGC	CAC	AAG	CTG	TCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	64			73			82			91			100			109		
	GGG	CAC	GCA	GCC	CCT	AGC	GGC	GCG	TCG	CTG	CCA	AGC	CGG	CCT	CCG	CGC	GCC	TCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	118			127			136			145			154			163		
	CTC	CTT	CCT	TCT	CCC	CTG	GCT	GTT	CGC	GAT	CCA	GCT	TGG	GTA	GGC	GGG	GAA	GCA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	172			181			190			199			208			217		
	GCT	GGA	GTG	CGA	CCG	CCA	CGG	CAG	CCA	CCC	TGC	AAC	CGC	CAG	TCG	GAG	GTG	CAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	226			235			244			253			262			271		
	TCC	GTA	GGC	CCT	GGC	CCC	CGG	GTG	GGC	CCT	TGG	GGA	GTC	GGC	GCC	GCT	CCC	GAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	280			289			298			307			316			325		
	GAG	CTG	CAA	GGC	TCG	CCC	CTG	CCC	GGC	GTG	GAG	GGC	GCG	GGG	GGC	GCG	GAG	GAT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	334			343			352			361			370			379		
	ATT	CTT	GGT	GAT	CTT	GGA	AGT	GTC	CGT	ATC	ATG	GAA	TCA	ATC	TCT	ATG	ATG	GGA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
											M	E	S	I	S	M	M	G
	388			397			406			415			424			433		
	AGC	CCT	AAG	AGC	CTT	AGT	GAA	ACT	TGT	TTA	CCT	AAT	GGC	ATA	AAT	GGT	ATC	AAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	S	P	K	S	L	S	E	T	C	L	P	N	G	I	N	G	I	K
	442			451			460			469			478			487		
	GAT	GCA	AGG	AAG	GTC	ACT	GTA	GGT	GTG	ATT	GGA	AGT	GGA	GAT	TTT	GCC	AAA	TCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	D	A	R	K	V	T	V	G	V	I	G	S	G	D	F	A	K	S
	496			505			514			523			532			541		
	TTG	ACC	ATT	CGA	CTT	ATT	AGA	TGC	GGC	TAT	CAT	GTG	GTC	ATA	GGA	AGT	AGA	AAT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	L	T	I	R	L	I	R	C	G	Y	H	V	V	I	G	S	R	N
	550			559			568			577			586			595		
	CCT	AAG	TTT	GCT	TCT	GAA	TTT	TTT	CCT	CAT	GTG	GTA	GAT	GTC	ACT	CAT	CAT	GAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	P	K	F	A	S	E	F	F	P	H	V	V	D	V	T	H	H	E
	604			613			622			631			640			649		
	GAT	GCT	CTC	ACA	AAA	ACA	AAT	ATA	ATA	TTT	GTT	GCT	ATA	CAC	AGA	GAA	CAT	TAT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	D	A	L	T	K	T	N	I	I	F	V	A	I	H	R	E	H	Y
	658			667			676			685			694			703		
	ACC	TCC	CTG	TGG	GAC	CTG	AGA	CAT	CTG	CTT	GTG	GGT	AAA	ATC	CTG	ATT	GAT	GTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	T	S	L	W	D	L	R	H	L	L	V	G	K	I	L	I	D	V
	712			721			730			739			748			757		
	AGC	AAT	AAC	ATG	AGG	ATA	AAC	CAG	TAC	CCA	GAA	TCC	AAT	GCT	GAA	TAT	TTG	GCT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	S	N	N	M	R	I	N	Q	Y	P	E	S	N	A	E	Y	L	A

TCA	TTA	766	CCA	GAT	775	TCT	TTG	ATT	784	GTC	AAA	GGA	793	TTT	AAT	GTT	802	GTC	TCA	GCT	811	TGG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
S	L	F	P	D	S	L	I	V	K	G	F	N	V	V	S	A	W						
GCA	CTT	820	CAG	TTA	GGA	CCT	AAG	GAT	838	GCC	AGC	CGG	847	CAG	GTT	TAT	856	ATA	TGC	AGC	865	AAC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
A	L	Q	L	G	P	K	D	A	S	R	Q	V	Y	I	C	S	N						
AAT	ATT	874	CAA	GCG	CGA	883	CAA	CAG	GTT	892	ATT	GAA	CTT	901	GCC	CGC	CAG	910	TTG	AAT	TTC	919	ATT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
N	I	Q	A	R	Q	Q	V	I	E	L	A	R	Q	L	N	F	I						
CCC	ATT	928	GAC	TTG	GGA	937	TCC	TTA	TCA	946	TCA	GCC	AGA	955	GAG	ATT	GAA	964	AAT	TTA	CCC	973	CTA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
P	I	D	L	G	S	L	S	S	A	R	E	I	E	N	L	P	<u>L</u>						
CGA	CTC	982	TTT	ACT	CTC	991	TGG	AGA	GGG	1000	CCA	GTG	GTG	1009	GTA	GCT	ATA	1018	AGC	TTG	GCC	1027	ACA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
<u>R</u>	<u>L</u>	<u>F</u>	<u>T</u>	<u>L</u>	<u>W</u>	<u>R</u>	<u>G</u>	<u>P</u>	<u>V</u>	<u>V</u>	<u>V</u>	<u>A</u>	<u>I</u>	<u>S</u>	<u>L</u>	<u>A</u>	<u>T</u>						
TTT	TTT	1036	TTC	CTT	TAT	1045	TCC	TTT	GTC	1054	AGA	GAT	GTG	1063	ATT	CAT	CCA	1072	TAT	GCT	AGA	1081	AAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
<u>F</u>	<u>F</u>	<u>F</u>	<u>L</u>	Y	S	F	V	R	D	V	I	H	P	Y	A	R	N						
CAA	CAG	1090	AGT	GAC	TTT	1099	TAC	AAA	ATT	1108	CCT	ATA	GAG	1117	ATT	GTG	AAT	1126	AAA	ACC	TTA	1135	CCT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Q	Q	S	D	F	Y	K	I	P	I	E	I	<u>V</u>	<u>N</u>	<u>K</u>	<u>T</u>	<u>L</u>	<u>P</u>						
ATA	GTT	1144	GCC	ATT	ACT	1153	TTG	CTC	TCC	1162	CTA	GTA	TAC	1171	CTT	GCA	GGT	1180	CTT	CTG	GCA	1189	GCT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
<u>I</u>	<u>V</u>	<u>A</u>	<u>I</u>	<u>T</u>	<u>L</u>	<u>L</u>	<u>S</u>	<u>L</u>	<u>V</u>	<u>Y</u>	<u>L</u>	<u>A</u>	<u>G</u>	<u>L</u>	<u>L</u>	<u>A</u>	<u>A</u>						
GCT	TAT	1198	CAA	CTT	TAT	1207	TAC	GGC	ACC	1216	AAG	TAT	AGG	1225	AGA	TTT	CCA	1234	CCT	TGG	TTG	1243	GAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A	Y	Q	L	Y	Y	G	T	K	Y	R	R	F	P	P	W	L	E						
ACC	TGG	1252	TTA	CAG	TGT	1261	AGA	AAA	CAG	1270	CTT	GGA	TTA	1279	CTA	AGT	TTT	1288	TTC	TTC	GCT	1297	ATG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	W	L	Q	C	R	K	<u>Q</u>	<u>L</u>	<u>G</u>	<u>L</u>	<u>L</u>	<u>S</u>	<u>F</u>	<u>F</u>	<u>F</u>	<u>A</u>	<u>M</u>						
GTC	CAT	1306	GTT	GCC	TAC	1315	AGC	CTC	TGC	1324	TTA	CCG	ATG	1333	AGA	AGG	TCA	1342	GAG	AGA	TAT	1351	TTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
<u>V</u>	<u>H</u>	<u>V</u>	<u>A</u>	<u>Y</u>	<u>S</u>	<u>L</u>	<u>C</u>	<u>L</u>	<u>P</u>	<u>M</u>	R	R	S	E	R	Y	L						
TTT	CTC	1360	AAC	ATG	GCT	1369	TAT	CAG	CAG	1378	GTT	CAT	GCA	1387	AAT	ATT	GAA	1396	AAC	TCT	TGG	1405	AAT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
F	L	N	M	A	Y	Q	Q	V	H	A	N	I	E	N	S	W	N						
GAG	GAA	1414	GAA	GTT	TGG	1423	AGA	ATT	GAA	1432	ATG	TAT	ATC	1441	TCC	TTT	GGC	1450	ATA	ATG	AGC	1459	CTT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
E	E	E	V	W	R	I	E	<u>M</u>	<u>Y</u>	<u>I</u>	<u>S</u>	<u>F</u>	<u>G</u>	<u>I</u>	<u>M</u>	<u>S</u>	<u>L</u>						

1468	1477	1486	1495	1504	1513
GGC TTA CTT TCC CTC	CTG GCA GTC ACT TCT ATC	CCT TCA GTG AGC AAT GCT	TTA		
<u>G L L S L L A V T S I P S</u>	<u>V S N A L</u>				
1522	1531	1540	1549	1558	1567
AAC TGG AGA GAA TTC AGT	TTT ATT CAG TCT ACA	CTT GGA TAT GTC GCT CTG	CTC		
<u>N W R E F S F I Q S T L G Y V A L L</u>					
1576	1585	1594	1603	1612	1621
ATA AGT ACT TTC CAT GTT	TTA ATT TAT GGA TGG	AAA CGA GCT TTT GAG GAA	GAG		
<u>I S T F H V L I Y G W K R A F E E E</u>					
1630	1639	1648	1657	1666	1675
TAC TAC AGA TTT TAT ACA	CCA CCA AAC TTT GTT	CTT GCT CTT GTT TTG CCC	TCA		
<u>Y Y R F Y T P P N F V L A L V L P S</u>					
1684	1693	1702	1711	1720	1729
ATT GTA ATT CTG GAT CTT	TTG CAG CTT TGC AGA	TAC CCA GAC TGA GCT GGA	ACT		
<u>I V I L D L L Q L C R Y P D *</u>					
1738	1747	1756	1765	1774	1783
GGA ATT TGT CTT CCT ATT	GAC TCT ACT TCT TTA	AAA GCG GCT GCC CAT TAC	ATT		
1792	1801	1810	1819	1828	1837
CCT CAG CTG TCC TTG CAG	TTA GGT GTA CAT GTG	ACT GAG TGT TGG CCA GTG	AGA		
1846	1855	1864	1873	1882	1891
TGA AGT CTC CTC AAA GGA	AGG CAG CAT GTG TCC	TTT TTC ATC CCT TCA TCT	TGC		
1900	1909	1918	1927	1936	1945
TGC TGG GAT TGT GGA TAT	AAC AGG AGC CCT GGC	AGC TGT CTC CAG AGG ATC	AAA		
1954	1963	1972	1981	1990	1999
GCC ACA CCC AAA GAG TAA	GGC AGA TTA GAG ACC	AGA AAG ACC TTG ACT ACT	TCC		
2008	2017	2026	2035	2044	2053
CTA CTT CCA CTG CTT TTC	CTG CAT TTA AGC CAT	TGT AAA TCT GGG TGT GTT	ACA		
2062	2071	2080	2089	2098	2107
TGA AGT GAA AAT TAA TTC	TTT CTG CCC TTC AGT	TCT TTA TCC TGA TAC CAT	TTA		
2116	2125	2134	2143	2152	2161
ACA CTG TCT GAA TTA ACT	AGA CTG CAA TAA TTC	TTT CTT TTG AAA GCT TTT	AAA		
2170	2179	2188	2197	2206	2215
GGA TAA TGT GCA ATT CAC	ATT AAA ATT GAT TTT	CCA TTG TCA ATT AGT TAT	ACT		
2224	2233	2242	2251	2260	2269
CAT TTT CCT GCC TTG ATC	TTT CAT TAG ATA TTT	TGT ATC TGC TTG GAA TAT	ATT		
2278	2287	2296	2305	2314	2323
ATC TTC TTT TTA ACT GTG	TAA TTG GTA ATT ACT	AAA ACT CTG TAA TCT CCA	AAA		
2332	2341	2350	2359	2368	2377
TAT TGC TAT CAA ATT ACA	CAC CAT GTT TTC TAT	CAT TCT CAT AGA TCT GCC	TTA		
2386	2395	2404	2413	2422	2431
TAA ACA TTT AAA TAA AAA	GTA CTA TTT AAT GAT	TTA AAA AAA AAA AAA	AAA		
2440	2449				
AAA AAA AAA AAA AAA	AA 3'				

FIG. 10A

1 CGAAACTTCC CTCTACCCGC CCGGCCCGCG GCGCGCACCG TTGGCGCTGG ACGCTTCCTC
 GCTTTGAAGG GAGATGGGCG GGCCGGGGCG CGCGCGTGGC AACC GCGACC TGCGAAGGAG

61 CTTGGAAGCG CCTCTCCCTC **AGTTATGGAG** M E K T C I D A L P L T
 GAACCTTCGC GGAGAGGGAG TCAATACCTC TTTTGAACAT ATCTACGTGA AGGAGAATGA

121 M N S S E K Q E T V C I F G T G D F G R
 ATGAATTCTT CAGAAAAGCA AGAGACTGTA TGTATTTTGT GAACTGGTGA TTTTGAAGA
 TACTTAAGAA GTCTTTTTCGT TCTCTGACAT ACATAAAAAAC CTTGACCACT AAAACCTTCT

181 S L G L K M L Q C G Y S V V F G S R N P
 TCACTGGGAT TGAAAATGCT CCAGTGTGGT TATTCTGTTG TTTTGGGAAG TCGAAACCCC
 AGTGACCCTA ACTTTTACGA GGTACACCA ATAAGACAAC AAAACCTTC AGCTTTGGGG

241 Q K T T L L P S G A E V L S Y S E A A K
 CAGAAGACCA CCCTACTGCC CAGTGGTGCA GAAGTCTTGA GCTATTCAGA AGCAGCCAAG
 GTCTTCTGGT GGGATGACGG GTCACCACGT CTTCAGAACT CGATAAGTCT TCGTCGGTTC

301 K S G I I I I A I H R E H Y D F L T E L
 AAGTCTGGCA TCATAATCAT AGCAATCCAC AGAGAGCATT ATGATTTTCT CACAGAATTA
 TTCAGACCGT AGTATTAGTA TCGTTAGGTG TCTCTCGTAA TACTAAAAGA GTGTCTTAAT

361 T E V L N G K I L V D I S N N L K I N Q
 ACTGAGGTTT TCAATGGAAA AATATTGGTA GACATCAGCA ACAACCTCAA AATCAATCAA
 TGACTCCAAG AGTTACCTTT TTATAACCAT CTGTAGTCGT TGTGGAGTT TTAGTTAGTT

421 Y P E S N A E Y L A H L V P G A H V V K
 TATCCAGAAT CTAATGCAGA GTACCTTGCT CATTTGGTGC CAGGAGCCCA CGTGGTAAAA
 ATAGGTCTTA GATTACGTCT CATGGAACGA GTAAACCACG GTCCTCGGGT GCACCATTTT

481 A F N T I S A W A L Q S G A L D A S R Q
 GCATTTAACA CCATCTCAGC CTGGGCTCTC CAGTCAGGAG CACTGGATGC AAGTCGGCAG
 CGTAAATTGT GGTAGAGTCG GACCCGAGAG GTCAGTCCTC GTGACCTACG TTCAGCCGTC

541 V F V C G N D S K A K Q R V M D I V R N
 GTGTTTGTGT GTGGAAATGA CAGCAAAGCC AAGCAAAGAG TGATGGATAT TGTTCTGTAAT
 CACAAACACA CACCTTTACT GTCGTTTCGG TTCGTTTCTC ACTACCTATA ACAAGCATTA

601 L G L T P M D Q G S L M A A K E I E K Y
 CTTGGACTTA CTCCAATGGA TCAAGGATCA CTCATGGCAG CCAAAGAAAT TGAAAAGTAC
 GAACCTGAAT GAGGTTACCT AGTTCCTAGT GAGTACCGTC GGTTTCTTTA ACTTTTCATG

661 P L Q L F P M W R F P F Y L S A V L C V
 CCCCTGCAGC TATTTCCAAT GTGGAGGTTT CCCTTCTATT TGTCTGCTGT GCTGTGTGTC
 GGGGACGTCG ATAAAGGTTA CACCTCCAAG GGGAAAGATA ACAGACGACA CGACACACAG

721 F L F F Y C V I R D V I Y P Y V Y E K K
 TTCTTGTTTT TCTATTGTGT TATAAGAGAC GTAATCTACC CTTATGTTTA TGAAAAGAAA
 AAGAACAAAA AGATAACACA ATATTCTCTG CATTAGATGG GAATACAAAT ACTTTTCTTT

D N T F R M A I S I P N R I F P I T A L
 781 GATAATACAT TTCGTATGGC TATTTCCATT CCAAATCGTA TCTTTCCAAT AACAGCACTT
 CTATTATGTA AAGCATACCG ATAAAGGTAA GGTTAGCAT AGAAAGGTTA TTGTCGTGAA

T L L A L V Y L P G V I A A I L Q L Y R
 841 ACACTGCTTG CTTTGGTTTA CCTCCCTGGT GTTATTGCTG CCATTCTACA ACTGTACCGA
 TGTGACGAAC GAAACCAAAT GGAGGGACCA CAATAACGAC GGTAAGATGT TGACATGGCT

G T K Y R R F P D W L D H W M L C R K Q
 901 GGCACAAAAT ACCGTCGATT CCCAGACTGG CTTGACCACT GGATGCTTTG CCGAAAGCAG
 CCGTGTTTTA TGGCAGCTAA GGGTCTGACC GAACTGGTGA CCTACGAAAC GGCTTTTCGTC

L G L V A L G F A F L H V L Y T L V I P
 961 CTTGGCTTGG TAGCTCTGGG ATTTGCCTTC CTTCATGTCC TCTACACACT TGTGATTCTT
 GAACCGAACC ATCGAGACCC TAAACGGAAG GAAGTACAGG AGATGTGTGA AACTAAGGA

I R Y Y V R W R L G N L T V T Q A I L K
 1021 ATTCGATATT ATGTACGATG GAGATTGGGA AACTTAACCG TTACCCAGGC AATACTCAAG
 TAAGCTATAA TACATGCTAC CTCTAACCTT TTGAATTGGC AATGGGTCCG TTATGAGTTC

K E N P F S T S S A W L S D S Y V A L G
 1081 AAGGAGAATC CATTTAGCAC CTCCTCAGCC TGGCTCAGTG ATTCATATGT GGCTTTGGGA
 TTCTCTTAG GTAAATCGTG GAGGAGTCGG ACCGAGTCAC TAAGTATACA CCGAAACCTT

I L G F F L F V L L G I T S L P S V S N
 1141 ATACTTGGGT TTTTCTGTT TGTACTCTTG GGAATCACTT CTTTGCCATC TGTTAGCAAT
 TATGAACCCA AAAAAGACAA ACATGAGAAC CCTTAGTGAA GAAACGGTAG ACAATCGTTA

A V N W R E F R F V Q S K L G Y L T L I
 1201 GCAGTCAACT GGAGAGAGTT CCGATTTGTC CAGTCCAAAC TGGGTTATTT GACCCTGATC
 CGTCAGTTGA CCTCTCTCAA GGCTAAACAG GTCAGGTTTG ACCCAATAAA CTGGGACTAG

L C T A H T L V Y G G K R F L S P S N L
 1261 TTGTGTACAG CCCACACCCT GGTGTACGGT GGAAGAGAT TCCTCAGCCC TTCAAATCTC
 AACACATGTC GGGTGTGGGA CCACATGCCA CCCTTCTCTA AGGAGTCGGG AAGTTTAGAG

R W Y L P A A Y V L G L I I P C T V L V
 1321 AGATGGTATC TTCCTGCAGC CTACGTGTTA GGGCTTATCA TTCCTTGAC TGTGCTGGTG
 TCTACCATAG AAGGACGTCG GATGCACAAT CCCGAATAGT AAGGAACGTG ACACGACCAC

I K F V L I M P C V D N T L T R I R Q G
 1381 ATCAAGTTTG TCCTAATCAT GCCATGTGTA GACAACACCC TTACAAGGAT CCGCCAGGGC
 TAGTTCAAAC AGGATTAGTA CGGTACACAT CTGTTGTGGG AATGTTCTTA GGCGGTCCCG

W E R N S K H
 1441 TGGGAAAGGA ACTCAAACA CTAGAAAAG CATTGAATGG AAAATCAATA TTAAAACAA
 ACCCTTTCCT TGAGTTTTGT GATCTTTTTC GTAACCTACC TTTTAGTTAT AAATTTTGTT

1501 AGTTCAATTT AGCTGGATTT CTGAACATATG GTTTTGAATG TTAAAGAAG AATGATGGGT
 TCAAGTAAA TCGACCTAAA GACTTGATAC CAAAACCTAC AAATTTCTTC TTACTACCCA

1561 ACAGTTAGGA AAGTTTTTTT CTTACACCGT GACTGAGGGA AACATTGCTT GTCTTTGAGA
 TGTCAATCCT TTCAAAAAA GAATGTGGCA CTGACTCCCT TTGTAACGAA CAGAACTCT

1621 AATTGACTGA CATACTGGAA GAGAACACCA TTTTATCTCA GGTTAGTGAA GAATCAGTGC
 TTAACGACT GTATGACCTT CTCTGTGGT AAAATAGAGT CCAATCACTT CTTAGTCACG

1681	AGGTCCCTGA	CTCTTATTTT	CCCAGAGGCC	ATGGAGCTGA	GATTGAGACT	AGCCTTGTGG
	TCCAGGGACT	GAGAATAAAA	GGGTCTCCGG	TACCTCGACT	CTAACTCTGA	TCGGAACACC
1741	TTTCACACTA	AAGAGTTTCC	TTGTTATGGG	CAACATGCAT	GACCTAATGT	CTTGCAAAAT
	AAAGTGTGAT	TTCTCAAAGG	AACAATACCC	GTTGTACGTA	CTGGATTACA	GAACGTTTTA
1801	CCAATAGAAG	TATTGCAGCT	TCCTTCTCTG	GCTCAAGGGC	TGAGTTAAGT	GAAAGGAAAA
	GGTTATCTTC	ATAACGTCGA	AGGAAGAGAC	CGAGTTCCCCG	ACTCAATTCA	CTTTCCTTTT
1861	ACAGCACAAT	GGTGACCACT	GATAAAGGCT	TTATTAGGTA	TATCTGAGGA	AGTGGGTCAC
	TGTCGTGTTA	CCACTGGTGA	CTATTTCCGA	AATAATCCAT	ATAGACTCCT	TCACCCAGTG
1921	ATGAAATGTA	AAAAGGGAAT	GAGGTTTTTG	TTGTTTTTTG	GAAGTAAAGG	CAAACATAAA
	TACTTTACAT	TTTTCCCTTA	CTCCAAAAAC	AACAAAAAAC	CTTCATTTCC	GTTTGTATTT
1981	TATTACCATG	ATGAATTCTA	GTGAAATGAC	CCCTTGACTT	TGCTTTTCTT	AATACAGATA
	ATAATGGTAC	TACTTAAGAT	CACTTTACTG	GGGAACTGAA	ACGAAAAGAA	TTATGTCTAT
2041	TTTACTGAGA	GGAACATTTT	TTATAACACA	AGAAAAATTT	ACAATTGATT	AAAAGTATCC
	AAATGACTCT	CCTTGATAAA	AATATTGTGT	TCTTTTTTAA	TGTTAACTAA	TTTTCATAGG
2101	ATGTCTTGGA	TACATACGTA	TCTATAGAGC	TGGCATGTAA	TTCTTCCTCT	ATAAAGAATA
	TACAGAACCCT	ATGTATGCAT	AGATATCTCG	ACCGTACATT	AAGAAGGAGA	TATTTCTTAT
2161	GGTATAGGAA	AGACTGAATA	AAAATGGAGG	GATATCCCCT	TGGATTTTAC	TTGCATTGTG
	CCATATCCCT	TCTGACTTAT	TTTTACCTCC	CTATAGGGGA	ACCTAAAGTG	AACGTAACAC
2221	CAATAAGCAA	AGAAGGGTTG	ATAAAAGTTC	TTGATCAAAA	AGTTCAAAGA	AACCAGAATT
	GTTATTCGTT	TCTTCCCAAC	TATTTTCAAG	AACTAGTTTT	TCAAGTTTCT	TTGGTCTTAA
2281	TTAGACAGCA	AGCTAAATAA	ATATTGTAAA	ATTGCACTAT	ATTAGGTTAA	GTATTATTTA
	AATCTGTCGT	TCGATTTATT	TATAACATTT	TAACGTGATA	TAATCCAATT	CATAATAAAT
2341	GGTATTATAA	TATGCTTTGT	AAATTTTATA	TTCCAAATAT	TGCTCAATAT	TTTTCATCTA
	CCATAATATT	ATACGAAACA	TTTAAAATAT	AAGGTTTATA	ACGAGTTATA	AAAAGTAGAT
2401	TTAAATTAAT	TTCTAGTGTA	AATAAGTAGC	TTCTATATCT	GTCTTAGTCT	ATTATAATTG
	AATTTAATTA	AAGATCACAT	TTATTCATCG	AAGATATAGA	CAGAATCAGA	TAATATTAAC
2461	TAAGGAGTAA	AATTAAATGA	ATAGTCTGCA	GGTATAAATT	TGAACAATGC	ATAGATGATC
	ATTCCTCATT	TTAATTTACT	TATCAGACGT	CCATATTTAA	ACTTGTTACG	TATCTACTAG
2521	GAAAAATTACG	GAAATCATA	GGGCAGAGAG	GTGTGAAGAT	TCATCATTAT	GTGAAATTTG
	CTTTTAATGC	CTTTTAGTAT	CCCGTCTCTC	CACACTTCTA	AGTAGTAATA	CACTTTAAAC
2581	GATCTTTCTC	AAATCCTTGC	TGAAATTTAG	GATGGTTCTC	ACTGTTTTTC	TGTGCTGATA
	CTAGAAAGAG	TTTAGGAACG	ACTTTAAATC	CTACCAAGAG	TGACAAAAAG	ACACGACTAT
2641	GTACCCTTTC	CAAGGTGACC	TTCAGGGGGA	TTAACCTTCC	TAGCTCAAGC	AATGAGCTAA
	CATGGGAAAG	GTTCCACTGG	AAGTCCCCCT	AATTGGAAGG	ATCGAGTTCC	TTACTCGATT
2701	AAGGAGCCTT	ATGCATGATC	TTCCACATA	TCAAAATAAC	TAAAAGGCAC	TGAGTTTGGC
	TTCTTCGGAA	TACGTACTAG	AAGGGTGTAT	AGTTTTATTG	ATTTTCCGTG	ACTCAAACCG
2761	ATTTTTCTGC	CTGCTCTGCT	AAGACCTTTT	TTTTTTTTTT	ACTTTCATTA	TAACATATTA
	TAAAAAGACG	GACGAGACGA	TTCTGGAAAA	AAAAAAAAAA	TGAAAGTAAT	ATTGTATAAT

2821	TACATGACAT	TATACAAAAA	TGATTAAAAT	ATATTAAAAC	AACATCAACA	ATCCAGGATA
	ATGTACTGTA	ATATGTTTTT	ACTAATTTTA	TATAATTTTG	TTGTAGTTGT	TAGGTCCTAT
2881	TTTTTCTATA	AAACTTTTTA	AAAATAATTG	TATCTATATA	TTCAATTTTA	CATCCTTTTT
	AAAAAGATAT	TTTGAAAAAT	TTTTATTAAAC	ATAGATATAT	AAGTTAAAAT	GTAGGAAAAA
2941	CAAAGGCTTT	GTTTTTCTAA	AGGCTTTGTT	TTCCTTTTTTA	TTATTTTTTTT	CTTTTTTTATT
	GTTTCCGAAA	CAAAAAGATT	TCCGAAACAA	AAGGAAAAAT	AATAAAAAAA	GAAAAAATAA
3001	TTTTTGAGAC	AGTCTTGCTC	TGTCGCTCAG	GCTGGAGTGC	AGTGGCACGA	TCTCAGCTCA
	AAAAACTCTG	TCAGAACGAG	ACAGCGAGTC	CGACCTCACG	TCACCGTGCT	AGAGTCGAGT
3061	CTGCAACCTC	CTCCTCCAG	GTTCAAGTGA	TTCTTGTTCA	TCAGCCTCCC	GAGTAGCTGG
	GACGTTGGAG	GAGGAGGGTC	CAAGTTCACT	AAGAACAAGT	AGTCGGAGGG	CTCATCGACC
3121	GACTACAGGC	ATGTGCCACT	ATGCCAGCT	AATTTTTGTA	CTTTTAGTAG	AGACAGGGTT
	CTGATGTCCG	TACACGGTGA	TACGGGTCTGA	TTAAAAACAT	GAAAATCATC	TCTGTCCCAA
3181	TCACCACATT	GGTCAGGCTG	GTCTTGAAAT	GCTGGCGTCA	AGTGATCTGC	CTGCCTCCGC
	AGTGGTGTA	CCAGTCCGAC	CAGAACTTTA	CGACCGCAGT	TCACTAGACG	GACGGAGGCG
3241	CTTACGTAAT	ATATTTTCTT	AATGGCTGCA	TAATATCACA	TCAAATAGGC	ATTTTTCAAA
	GAATGCATTA	TATAAAAGAA	TTACCGACGT	ATTATAGTGT	AGTTTATCCG	TAAAAAGTTT
3301	CCTCTTTCCT	TATTAAACAT	GTAGACTATA	TCCATTTTTT	ACTAAAATAA	ATAACATTTT
	GGAGAAAAGGA	ATAATTTGTA	CATCTGATAT	AGGTAAAAAA	TGATTTTATT	TATTGTAAAG
3361	AGATAATATC	TTTGCCTGTA	TAATGTTGCC	AAGCCATTTT	TAAAGTGACC	TTATCAATTT
	TCTATTATAG	AAACGTGACT	ATTACAACGG	TTCGGTAAAG	ATTTCACTGG	AATAGTTAAA
3421	AATTACCATT	GGATGAGGGT	GTTGCTTTCA	TCGCACCATT	GTAGATTGTC	TTTTTTATTT
	TTAATGGTAA	CCTACTCCCA	CAACGAAAGT	AGCGTGGTAA	CATCTAACAG	AAAAAATAAA
3481	CAATTTGCGT	TTATTTATAA	CTGGTTGCAA	AGGTACACAG	AACACACGCT	CCTTCAACTT
	GTTAAACGCA	AATAAATATT	GACCAACGTT	TCCATGTGTC	TTGTGTGCGA	GGAAGTTGAA
3541	ATCTTTGATA	AACCCAAGCA	AGGATACAAA	AAGTTGGACG	ACATTGAGTA	GAGTCATGGT
	TAGAACTAT	TTGGGTTTCGT	TCCTATGTTT	TTCAACCTGC	TGTAATCAT	CTCAGTACCA
3601	ATACGGTGCT	GACCCTACAG	TATCAGTGGA	AAAGATAAGG	AAAATGTCAC	TACTCACCTA
	TATGCCACGA	CTGGGATGTC	ATAGTCACCT	TTTCTATTCC	TTTACAGTG	ATGAGTGGAT
3661	TGTTATGCAA	AACAGTTAGG	TGTGCTGGGG	CTGGATACTG	CTCTTTTACT	TGAGCATTGG
	ACAATACGTT	TTGTCAATCC	ACACGACCCC	GACCTATGAC	GAGAAAATGA	ACTCGTAACC
3721	TTGATTAAAG	TTTAGGTACC	ATCCAGGCTG	GTCTAGAGAA	GTCTTTGGAG	TTAACCATGC
	AACTAATTTT	AAATCCATGG	TAGGTCCGAC	CAGATCTCTT	CAGAAACCTC	AATTGGTACG
3781	TCTTTTTGTT	AAAGAAGAGA	GTAATGTGTT	TATCCTGGCT	CATAGTCCGT	CACCGAAAAT
	AGAAAAACAA	TTTCTTCTCT	CATTACACAA	ATAGGACCGA	GTATCAGGCA	GTGGCTTTTA
3841	AGAAAATGCC	ATCCATAGGT	AAAATGCTGA	CCTATAGAAA	AAAATGAACT	CTACTTTTAT
	TCTTTTACGG	TAGGTATCCA	TTTTACGACT	GGATATCTTT	TTTACTTGA	GATGAAAATA
3901	AGCCTAGTAA	AAATGCTCTA	CCTGAGTAGT	TAAAAGCAAT	TCATGAAGCC	TGAAGCTAAA
	TCGGATCATT	TTTACGAGAT	GGACTCATCA	ATTTTCGTTA	AGTACTTCGG	ACTTCGATTT

3961 GAGCACTCTG ATGGTTTTGG CATAATAGCT GCATTTCCAG ACCTGACCTT TGGCCCCAAC
CTCGTGAGAC TACCAAAACC GTATTATCGA CGTAAAGGTC TGGACTGGAA ACCGGGGTTG

4021 CACAAGTGCT CCAAGCCCCA CCAGCTGACC AAAGAAAGCC CAAGTTCTCC TTCTGTCCTT
GTGTTACGA GGTTCTGGGT GGTCGACTGG TTTCTTTCGG GTTCAAGAGG AAGACAGGAA

4081 CCCACAACCT CCCTGCTCCC AAAACTATGA AATTAATTTG ACCATATTAA CACAGCTGAC
GGGTGTTGGA GGGACGAGGG TTTTGATACT TTAATTAAAC TGGTATAATT GTGTCGACTG

4141 TCCTCCAGTT TACTTAAGGT AGAAAGAATG AGTTTACAAC AGATGAAAAT AAGTGCTTTG
AGGAGGTCAA ATGAATTCCA TCTTTCTTAC TCAAATGTTG TCTACTTTTA TTCACGAAAC

4201 GGCGAACTGT ATTCCTTTTA ACAGATCCAA ACTATTTTAC ATTTAAAAAA AAAGTTAAAC
CCGCTTGACA TAAGGAAAAT TGTCTAGGTT TGATAAAATG TAAATTTTTT TTTCAATTTG

4261 TAAACTTCTT TACTGCTGAT ATGTTTCCTG TATTCTAGAA AAATTTTTTAC ACTTTCACAT
ATTTGAAGAA ATGACGACTA TACAAAGGAC ATAAGATCTT TTAAAAATG TGAAAGTGTA

4321 TATTTTTGTA CACTTTCCTC ATGTTAAGGG ATGATGGCTT TTATAAATGT GTATTCATTA
ATAAAAAACAT GTGAAAGGGG TACAATTCCC TACTACCGAA AATATTTACA CATAAGTAAT

4381 AATGTTACTT TAAAAATAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
TTACAATGAA ATTTTATTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

FIG. 10B

STEAP-2, AA508880 (NCI_CGAP Pr6)

ggtcgacttttccctttattcctttgtcagagatctgattcatccatgctagaaaccaacagagtgcacttttaca
aaattccctatagagattgtgaataaaaaccttacctatagttgccattactttgctctccctagtataccttgccagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggttggaacctgggta
cagtgtagaaaacagcttggtactaagttggttcttcgctatggtccatgttgctacagcctctgcttaccga
tgagaaggtcagagagat

STEAP-2, 98P4B6 SSH fragment

TTTGAGCTTTGCAGATACCCAGACTGAGCTGGAAC TGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAAGCG
GCTGCCCATTTACATTCCTCAGCTGTCTTGAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT

STEAP-3, A1139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttggggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcaactggagagagttccgatttgt
ccagtcctaaactgggttatttgacctgatcttgtgtacagccacacctgggtgtacggtgggaagagattcctc
agcccttcaaactctcagatgggtatcttctcgcagcctacgtgttagggcttatcattccttgactgtgctgggta
tcaagtttgcctaataatcatgccatgtgtagacaacaccttacaaggatccgccagggtgggaaaggaactcaa
acactagaaaaagcattgaatggaaaatcaatatataaaacaaagttcaatttagctggaaaaaaaaa

STEAP 4, R80991 (placental EST)

ggccgcggcanccgctacgacctgggtcaacctggcagtcaggcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggtatggagatctacctctccctgggagtgctggccctcggcacgttgcctgctggccg
tgacctcactgccgtccattgcaaaactcgtcaactggagggagttcagcttcgttcagtcctcactgggctttgt
ggccttcgtgctgagcacactncacacgctcacctacggctggacccgcgccttcgaggagagccgctacaagttc
tacctnctcccaaccttcacgntcacgctgctgggtgccctgcgttcgttcacctgggccaagccctgtttntac
tgcttgcattcagccgnaga

[illegible]

	361	375	376	390	391	405	406	420	421	435	436	450
2 STEAP2	IEMNISPQMSLGL	SLDAVTSIPSVSNAL	NWREFSPQSTIGV	ATLISHFVLYGK	RAFEERYRXTPPN	EVLAIVLE	-SIVILD	445				
3 STEAP3	SDSVAIGELGFTUF	VHGGTSLPSVSNV	NWREFRKYOSKGL	TYILCUAHTVNGCK	RFLSPSNLRWGPAA	YVIGLILIPCTVLVI	434					
4 STEAP1	KEIKVSLGTFVGHAI	ALCAVTSIPSVSDSI	TWREFHYIQSKLGI	SLHGGHIALIPAWN	KWIDIKQFVWTEPPT	EMIAVFEHIVVLEPK	305					
5 STEAP4	MEIKVSLGVIALGTI	SLDAVTSIPSVANSI	NWREFSVQSSLGFW	AXVLSLHTITTCWT	RAFEESRKYEXLPPA	FTXTTLVE-CWRSSW	120					

	451	465	466	480	481
2 STEAP2	LLQICRYPD	---	---	---	---
3 STEAP3	FVHIMPQVDNLTTRH	ROGWERNKH	---	---	454
4 STEAP1	SIHFLPGLRKKILKE	RHGWEDVTXINKTEI	CSQL	---	459
5 STEAP4	AKAFIXLFCIQPX	---	---	---	339
					133

FIG. 11B

STRAP-1 67 LFPQWHLPIKIAAIIASLTFLYTLTREVIHPLATSHQQYFYKIPILVINKVLEPMVSITLL
STRAP-2 208 LFTLWRGPVVVAISLATFFFYLFYFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLL
* * * * *
STRAP-1 127 ALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFVAVLHAIYSLSYPMRR
STRAP-2 268 SLVYLAGLLAAAYQLYYGTKYRRFPWLETWLQCRKQLGLLSFFFAMVHVAYSICLPMRR
* * * * *
STRAP-1 187 SYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLT
STRAP-2 328 SERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALN
* * * * *
STRAP-1 247 WREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLII
STRAP-2 388 WREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYRFEYTPPNFVLALVLPISIVIL
* * * * *

FIG. 11C

STEAP1 66 ELFPQWHLPIKIAAIIASLTFLYTLREVIHPLATSHQQYFYKIPILVINKVLPMSITL

STEAP3 195 QLFPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTL
*** * * * * * * * * * *

STEAP1 126 LALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFVAVLHAIYSLSPMR

STEAP3 255 LALVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIR
***** ** * * * * * * * * * *

STEAP1 186 RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVDSL

STEAP3 315 YYVRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLSVSNV
* * * * * * * * * *

STEAP1 246 TWREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMAVFLPIVVLIFK

STEAP3 375 NWREFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAAYVLGLIIPCTVLVIK
**** * * * * * * * * *

STEAP1 306 SILFLPCLRKKILKIRHWEDVTK

STEAP3 435 FVLIMPCVDNTLTRIRQGWERNK
* * * * *

FIG. 11D

STEAP2 29 RKVTVGVIGSGDFAKSLTIRLIRCGYHVIGSRNPKFASEFFPHVVDVTHHEDALTKTNI

STEAP3 18 KQETVCIFGTGDFGRSLGLKMLQCGYSVVFGSRNPQ-KTTLLPSGAEVLSYSEAAKSGI
 ** * *** ** *** ** * * *

STEAP2 89 IFVAIHREHYTSLWDLRHLLVGKILIDVSNMNRINQYPESNAEYLASLFPDSLIVKGFNV

STEAP3 77 IIIAIIHREHYDFLTEVLNGKILVDISNNLKINQYPESNAEYLAHLVPGAHVVKAFNT
 * * * * * * * * * * * * * * * * *

STEAP2 149 VSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIIDLGLSSAREIENLPLRL

STEAP3 137 ISAWALQSGALDASRQVFVCGNDSKAKQVRMDIVRNGLTPMDQGSLMAAKEIEKYPLQL
 * * * * * * * * * * * * * * * * *

STEAP2 209 FTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLLS

STEAP3 197 FPMWRFPFYLSAVLCVFLFFYCVIRDVIYPYVYEKKDNTFRMAISIPNRIFPITALTLLA
 * * * * * * * * * * * * * * * *

STEAP2 269 LVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSCLCLPMRRS

STEAP3 257 LVYLPGVIAAILQLYRGTKYRRFPDWLDHWMLCRKQLGLVALGFAFLHVLYTLVIPIRYY
 * * * * * * * * * * * * * * * *

STEAP2 329 ERYLFLNMAYQQVHANIEANSWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNW

STEAP3 317 VRWRLGNLTVTQAILKKENPFSTSSAWLSDSYVALGILGFFLFVLLGITSLSPSVSNVNW
 * * * * * * * * * * * * * * * *

STEAP2 389 REFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYRFYTPPNFVLALVLPISIVIL

STEAP3 377 REFRFVQSKLGYLTLILCTAHTLVYGGKRFLSPSNLRWYLPAAAYVLGLIIPCTVLV
 * * * * * * * * * * * * * * * *

FIG. 12A

Panel 1.

Heart
Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas

Panel 2.

Spleen
Thymus
Prostate
Testes
Ovary
Small Intestine
Colon
White Blood Cell

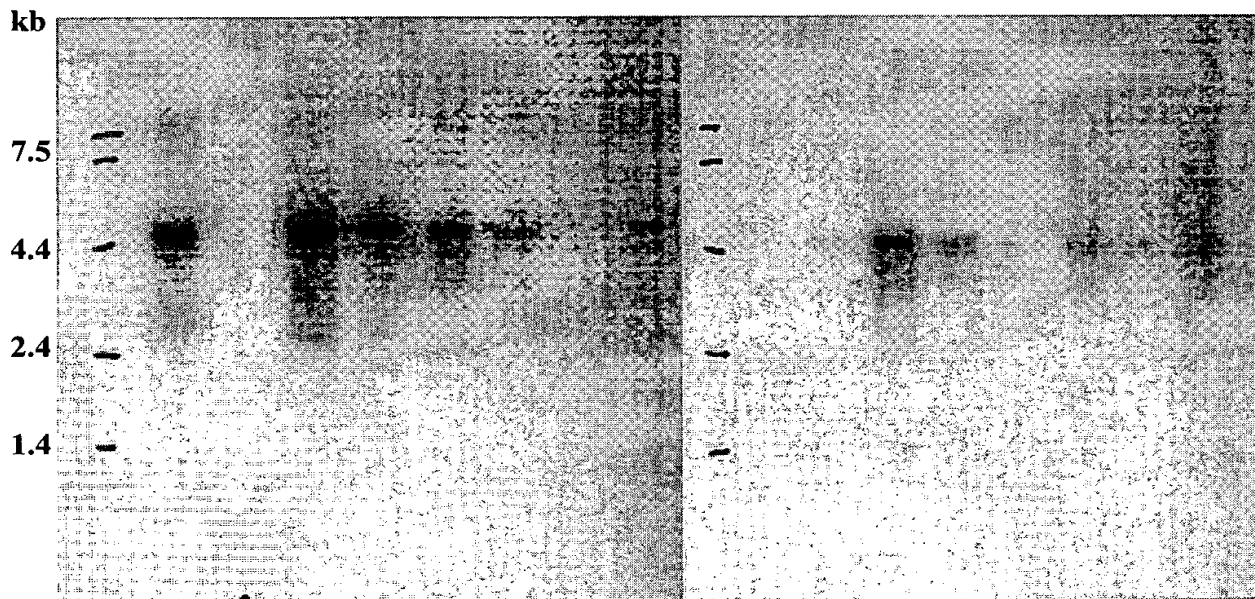
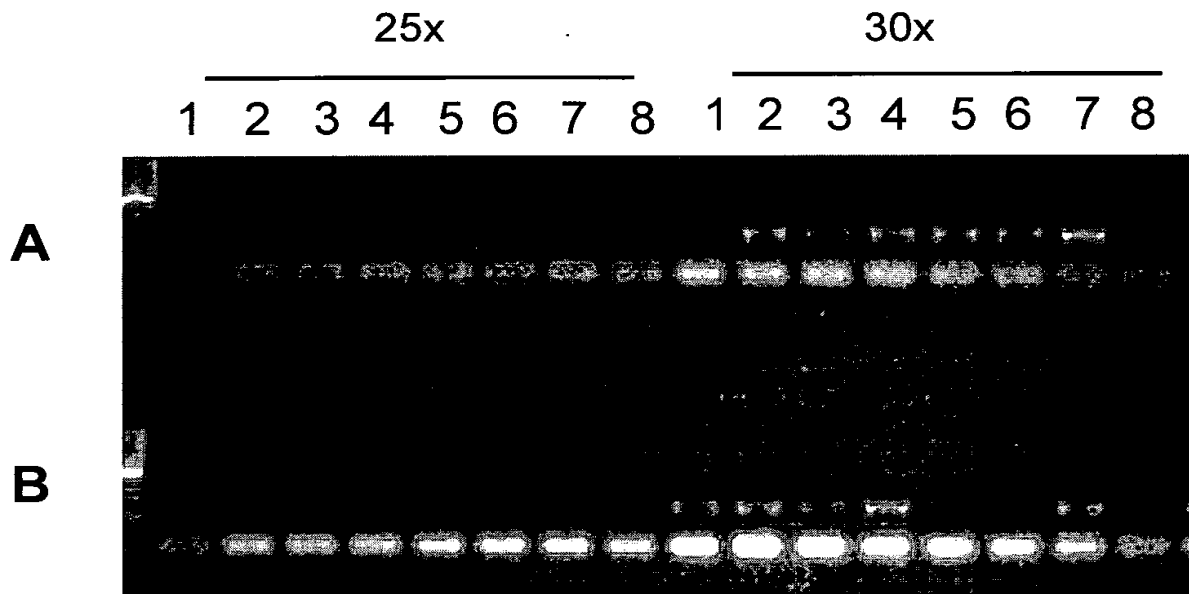


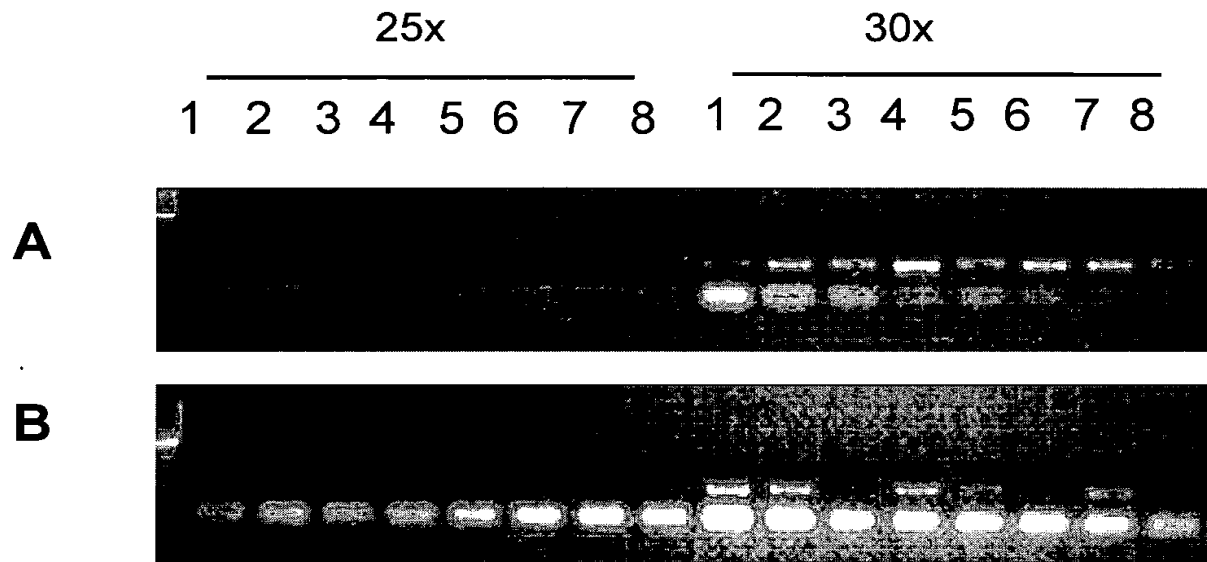
FIG. 12B



- A**
1. Brain
 2. Heart
 3. Kidney
 4. Liver
 5. Lung
 6. Pancreas
 7. Placenta
 8. Skeletal Muscle

- B**
1. Colon
 2. Ovary
 3. Leukocytes
 4. Prostate
 5. Small Intestine
 6. Spleen
 7. Testis
 8. Thymus

FIG. 13



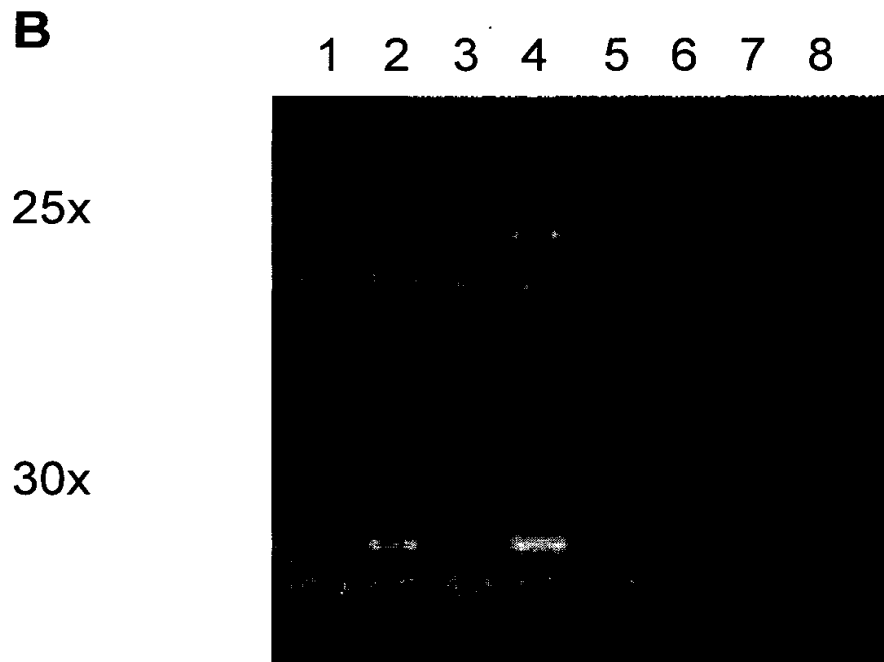
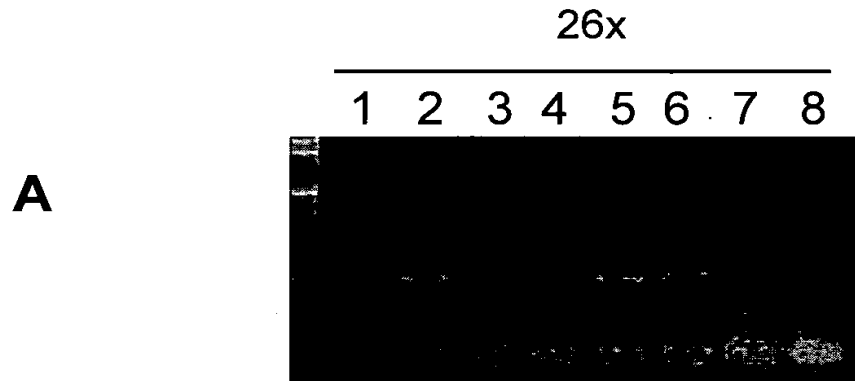
A

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

B

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG.14



- A**
1. Brain
 2. Prostate
 3. LAPC-4 AD
 4. LAPC-4 AI
 5. LAPC-9 AD
 6. HeLa
 7. Murine cDNA
 8. Neg. control

- B**
1. Colon
 2. Ovary
 3. Leukocytes
 4. Prostate
 5. Small Intestine
 6. Spleen
 7. Testis
 8. Thymus

FIG. 15

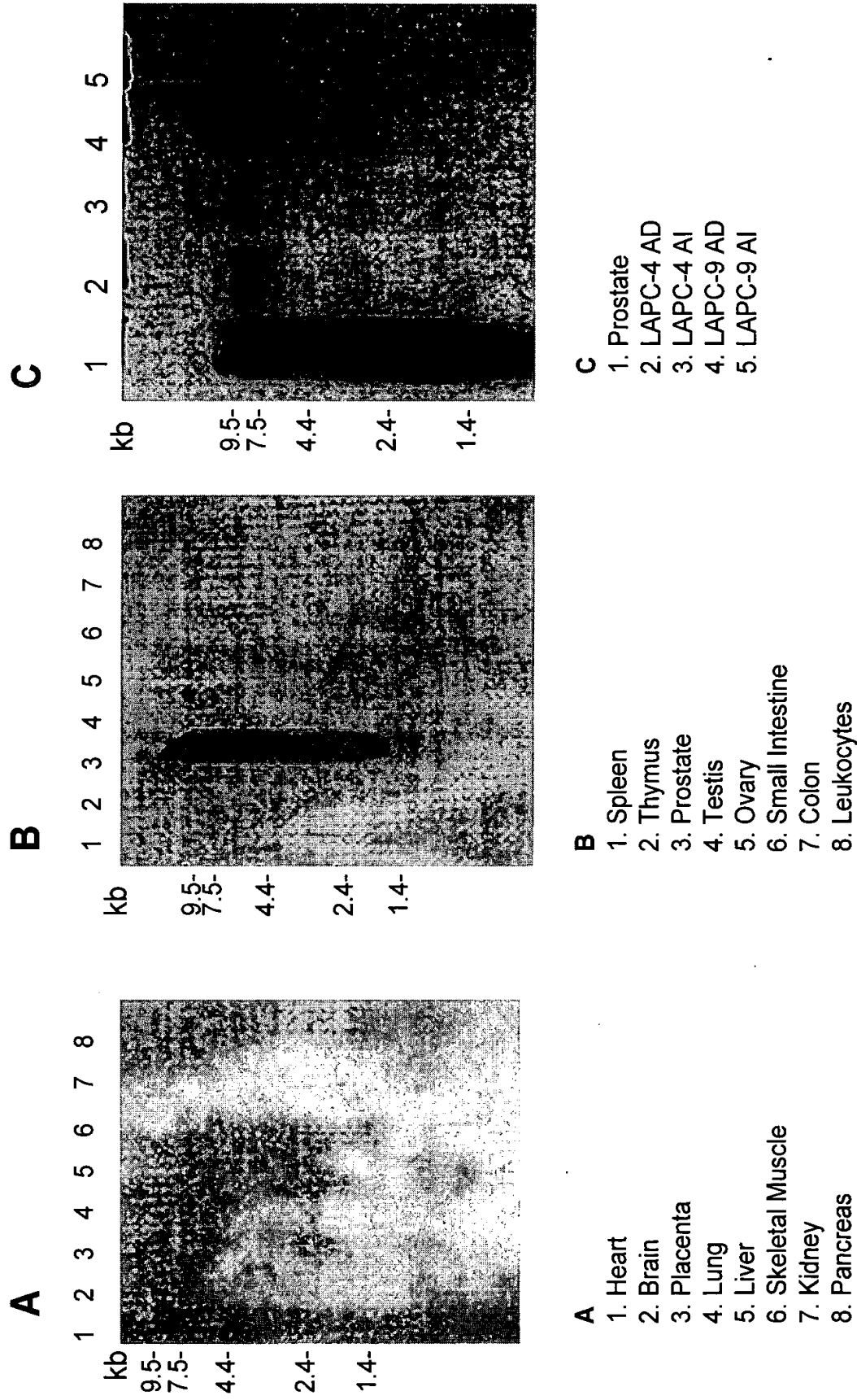


FIG. 16

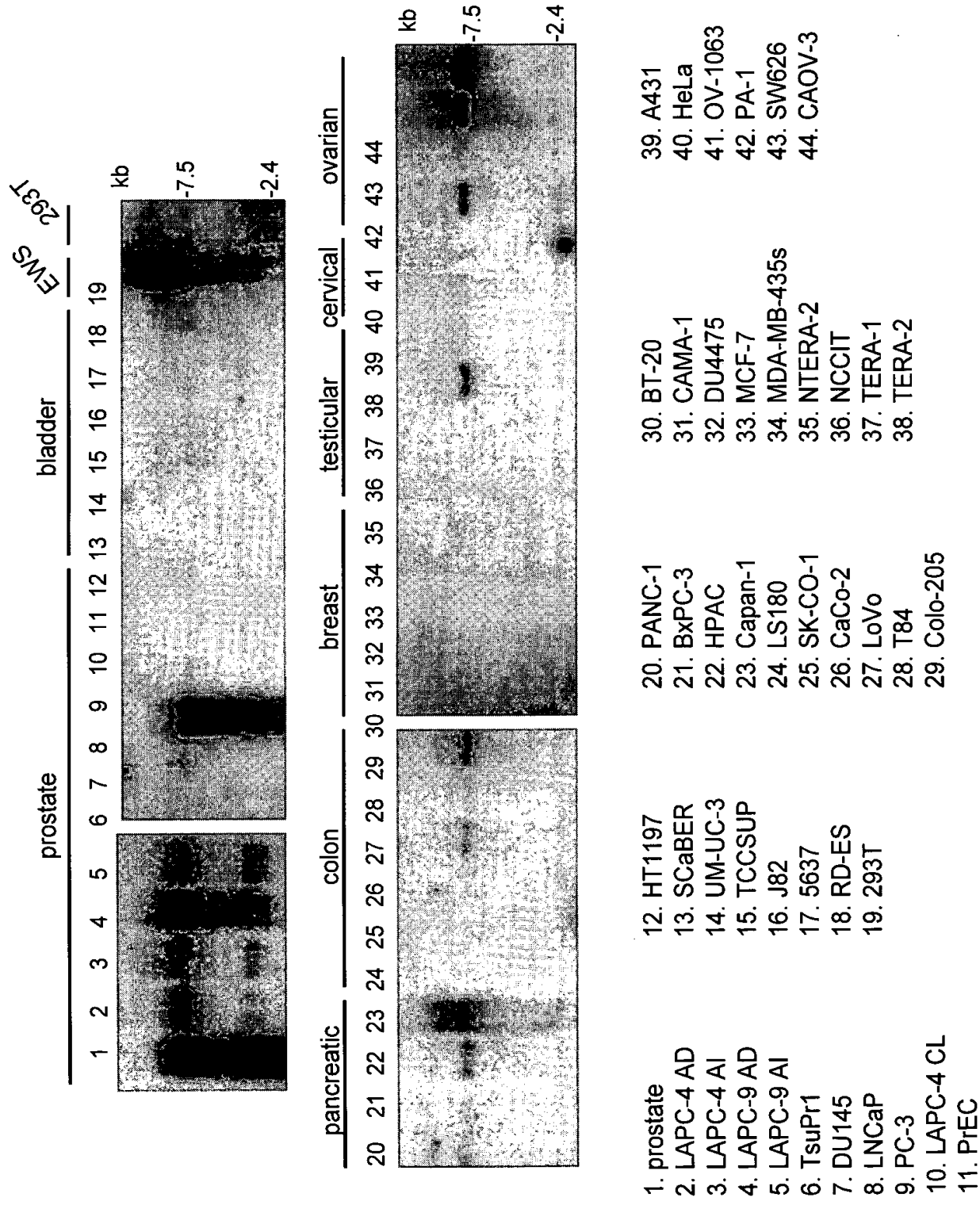


FIG. 17

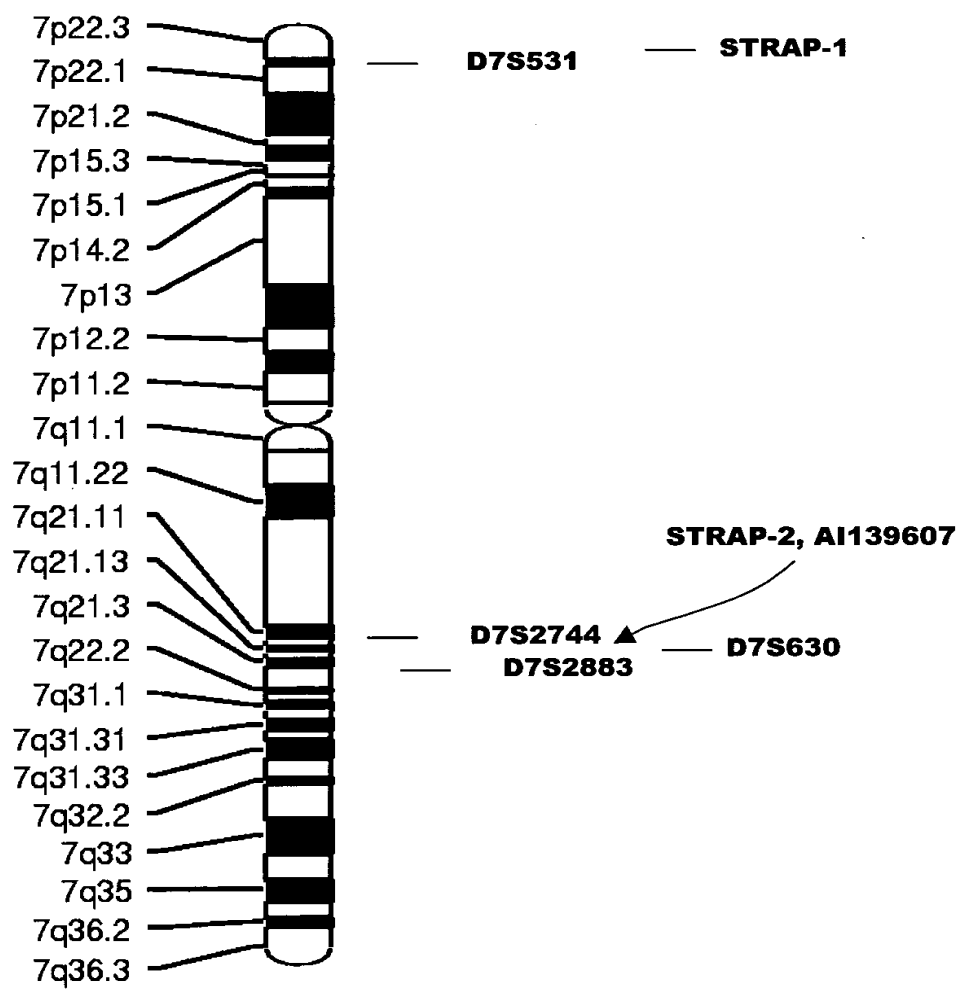


FIG. 18



FIG. 19

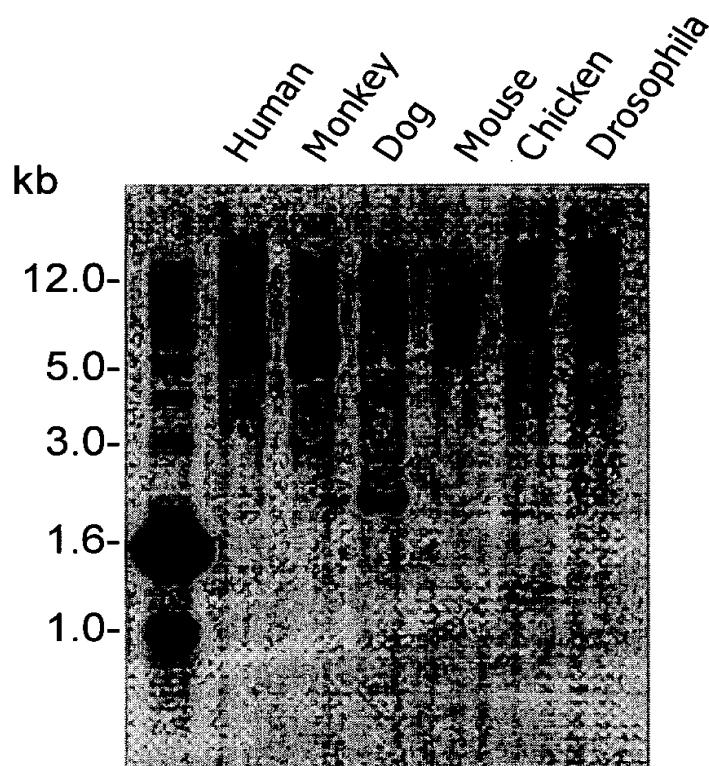
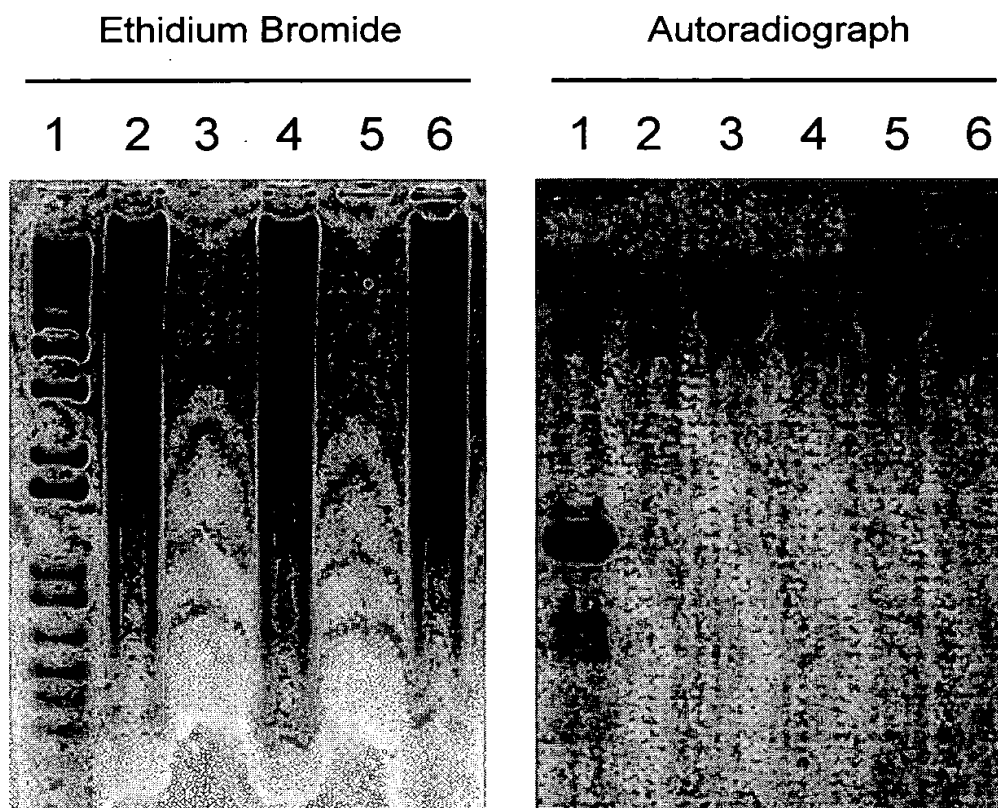


FIG. 20



Lanes

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3